

**G. SEQUENCE LISTING**

5 (1) **GENERAL INFORMATION**

(i) **APPLICANT:** Darrell Anderson, Nabil Hanna, John Leonard, Roland Newman and Mitchell Reff and William H. Rastetter

10 (ii) **TITLE OF INVENTION:** THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL LYMPHOMA

15 (iii) **NUMBER OF SEQUENCES:** 8

20 (iv) **CORRESPONDING ADDRESS:**

(A) **ADDRESSEE:** IDEC Pharmaceuticals Corporation  
(B) **STREET:** 11011 Torreyana Road  
(C) **CITY:** San Diego  
(D) **STATE:** California  
(E) **COUNTRY:** USA  
(F) **ZIP:** 92121

25 (v) **COMPUTER READABLE FORM:**

30 (A) **MEDIUM/TYPE:** Diskette, 3.5 inch, 1.44 Mb  
(B) **COMPUTER:** Macintosh  
(C) **OPERATING SYSTEM:** MS.DOS  
(D) **SOFTWARE:** Microsoft Word 5.0

35 (vi) **CURRENT APPLICATION DATA:**

40 (A) **APPLICATION NUMBER:**  
(B) **FILING DATE:**  
(C) **CLASSIFICATION:**

(vii) **ATTORNEY/AGENT INFORMATION:**

45 (A) **NAME:** Burgoon, Richard P. Jr.  
(B) **REGISTRATION NUMBER:** 34,787  
(C) **REFERENCE/DOCKET NUMBER:**

(ix) **TELECOMMUNICATION INFORMATION:**

50 (A) **TELEPHONE:** (619) 550-8500  
(B) **TELEFAX:** (619) 550-8750

(2) INFORMATION FOR SEQ ID NO: 1:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8540 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

B  
(iii) HYPOTHETICAL: <sup>NO</sup> <sub>yes</sub>

15 (iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

20	GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG	60
	AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC	120
	GGAGAATGGG CGGAACCTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT	180
25	ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG	240
	GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT	300
30	GGGGAGCCTG GGGACTTTCC ACACCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT	360
	AGTTATTAAT AGTAATCAAT TACGGGTCA TTAGTTCAT A GCCCATATAT GGAGTTCCGC	420
	GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG	480
35	ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTCCA TTGACGTCAA	540
	TGGGTGGACT ATTTACGCTA AACTGCCAC TTGGCAGTAC ATCAAGTGT A TCATATGCCA	600
40	AGTACGCCAC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT A TGCCAGTAC	660
	ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC	720
	ATGGTGATGC GGTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGA	780
45	TTTCCAAGTC TCCACCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG	840
	GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGCGG TAGGCGTGT	900
50	CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCCG CTGGAGACGC	960
	CATCACAGAT CTCTCACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG	1020
	CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA	1080
55	TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACCTGC CTCTGTTGTG	1140
	TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAAGGT GGATAACGCC	1200
60	CTCCAATCGG GTAACTCCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC	1260

	AGCCTCAGCA	GCACCCCTGAC	GCTGAGCAAA	GCAGACTACG	AGAAACACAA	AGTCTACGCC	1320
	TGCAGAAGTCA	CCCATCAGGG	CCTGAGCTCG	CCCCTCACAA	AGAGCTTCAA	CAGGGGAGAG	1380
5	TGTTGAATTG	AGATCCGTTA	ACGGTTACCA	ACTACCTAGA	CTGGATTCTG	GACAACATGC	1440
	GGCCGTGATA	TCTACGTATG	ATCAGCCTCG	ACTGTGCCTT	CTAGTTGCCA	GCCATCTGTT	1500
10	GTTTGCCCCCT	CCCCCGTGCC	TTCCCTTGACC	CTGGAAGGTG	CCACTCCCAC	TGTCCCTTCC	1560
	TAATAAAATG	AGGAAATTGC	ATCGCATTGT	CTGAGTAGGT	GTCATTCTAT	TCTGGGGGGT	1620
	GGGGTGGGGC	AGGACAGCAA	GGGGGAGGAT	TGGGAAGACA	ATAGCAGGCA	TGCTGGGGAT	1680
15	GCGGTGGGCT	CTATGGAACC	AGCTGGGCT	CGACAGCTAT	GCCAAGTACG	CCCCCTATTG	1740
	ACGTCAATGA	CGGTAAATGG	CCCGCCTGGC	ATTATGCCA	GTACATGACC	TTATGGGACT	1800
20	TTCCTACTTG	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG	ATGCGGTTTT	1860
	GGCAGTACAT	CAATGGCGT	GGATAGCGGT	TTGACTCACG	GGGATTTCGA	AGTCTCCACC	1920
	CCATTGACGT	CAATGGGAGT	TTGTTTGCG	ACCAAAATCA	ACGGGACTTT	CCAAAATGTC	1980
25	GTAACAACTC	CGCCCCATTG	ACGAAATGG	GCGGTAGGCG	TGTACGGTGG	GAGGTCTATA	2040
	TAAGCAGAGC	TGGGTACGTC	CTCACATTCA	GTGATCAGCA	CTGAACACAG	ACCCGTCGAC	2100
30	ATGGGTTGGA	GCCTCATCTT	GCTCTCCCTT	GTCGCTGTTG	CTACGCGTGT	CGCTAGCACC	2160
	AAGGGCCCAT	CGGTCTTCCC	CCTGGCACCC	TCCTCCAAGA	GCACCTCTGG	GGGCACAGCG	2220
	GCCCTGGGCT	GCCTGGTCAA	GGACTACTTC	CCCGAACCGG	TGACGGTGTG	GTGGAACACTA	2280
35	GGCGCCCTGA	CCAGCGCGT	GCACACCTTC	CCGGCTGTCC	TACAGTCCTC	AGGACTCTAC	2340
	TCCCTCAGCA	CGGTGGTGAC	CGTGCCTCC	AGCAGCTTGG	GCACCCAGAC	CTACATCTGC	2400
40	AACGTGAATC	ACAAGCCCAG	CAACACCAAG	GTGGACAAGA	AAGCAGAGCC	CAAATCTTGT	2460
	GACAAAATC	ACACATGCC	ACCGTGCCA	GCACCTGAAC	TCCTGGGGGG	ACCGTCAGTC	2520
	TTCCTCTTCC	CCCCAAAACC	CAAGGACACC	CTCATGATCT	CCCGGACCCC	TGAGGTCACA	2580
45	TGGCGGGTGG	TGGACGTGAG	CCACGAAGAC	CCTGAGGTCA	AGTTCAACTG	GTACGTGGAC	2640
	GGCGTGGAGG	TGCATAATGC	CAAGACAAG	CCGCGGGAGG	AGCAGTACAA	CAGCACGTAC	2700
50	CGTGTGGTCA	GCCTCCTCAC	CGTCCTGCAC	CAGGACTGGC	TGAATGGCAA	GGAGTACAAG	2760
	TGCAAGGTCT	CCAACAAAGC	CCTCCCAGCC	CCCATCGAGA	AAACCATCTC	CAAAGCCAAA	2820
	GGGCAGCCCC	GAGAACACAA	GGTGTACACC	CTGCCCCAT	CCCGGGATGA	GCTGACCAAG	2880
55	AACCAGGTCA	GCCTGACCTG	CCTGGTCAA	GGCTTCTATC	CCAGCGACAT	CGCCGTGGAG	2940
	TGGGAGAGCA	ATGGGCAGCC	GGAGAACAAAC	TACAAGACCA	CCGCTCCCGT	GCTGGACTCC	3000
60	GACGGCTCCT	TCTTCCTCTA	CAGCAAGCTC	ACCGTGGACA	ACAGCAGGTG	GCAGCAGGGG	3060
	AACGTCTTCT	CATGCTCCGT	GATGCATGAG	GCTCTGCACA	ACCACTACAC	GCAGAACAGC	3120
	CTCTCCCTGT	CTCCGGTAA	ATGAGGATCC	GTAAACGGTT	ACCAACTACC	TAGACTGGAT	3180

	TCGTGACAAC	ATGCGGCCGT	GATATCTACG	TATGATCAGC	CTCGACTGTG	CCTTCTAGTT	3240
5	GCCAGCCATC	TGTTGTTGCG	CCCTCCCCCG	TGCCTTCCTT	GACCTGGAA	GGTGCCACTC	3300
	CCACTGTCCT	TTCTTAATAA	AATGAGGAAA	TTGCATCGCA	TTGTCTGAGT	AGGTGTCATT	3360
							3360
10	GGCATGCTGG	GGATGCGGTG	GGCTCTATGG	AACCAGCTGG	GGCTCGACAG	CGCTGGATCT	3480
	CCCGATCCCC	AGCTTGCTT	CTCAATTCT	TATTCGCATA	ATGAGAAAAA	AAGGAAAATT	3540
15	AATTTTAACA	CCAATTCACT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAAG	GATGCTTCTAG	3600
	AGACAGTGT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	3660
	GACTCCTAAG	CCAGTGAGTG	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	3720
20	GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	3780
	GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTTGCTCCTC	ACATTGCTT	3840
25	CTGACATAGT	TGTGTTGGGA	GCTTGGATAG	CTTGGACAGC	TCAGGGCTGC	GATTCGCGC	3900
	CAAACCTGAC	GGCAATCCTA	GGGTGAAGGC	TGGTAGGATT	TTATCCCCGC	TGCCATCATG	3960
	GTTCGACCAT	TGAACCTGCAT	CGTCGCCGTG	TCCCAAAATA	TGGGGATTGG	CAAGAACGGA	4020
30	GACCTACCCCT	GGCCTCGCT	CAGGAACGAG	TTCAAGTACT	TCCAAAGAAT	GACCACAAACC	4080
	TCTTCAGTGG	AAGGTAAACA	GAATCTGGTG	ATTATGGTA	GGAAAACCTG	GTTCTCCATT	4140
	CCTGAGAAGA	ATCGACCTTT	AAAGGACAGA	ATTAATATAG	TTCTCAGTAG	AGAACTCAAA	4200
35	GAACCACCAAC	GAGGAGCTCA	TTTTCTTGCC	AAAAGTTGG	ATGATGCCTT	AAGACTTATT	4260
	GAACAACCGG	AATTGGCAAG	TAAAGTAGAC	ATGGTTTGG	TAGTCGGAGG	CAGTTCTGTT	4320
40	TACCAGGAAG	CCATGAATCA	ACCAGGCCAC	CTTAGACTCT	TTGTGACAAG	GATCATGCAG	4380
	GAATTGAAA	GTGACACGTT	TTTCCCAGAA	ATTGATTGG	GGAAATATAA	ACTTCTCCCA	4440
45	GAATACCCAG	CGTCCTCTC	TGAGGTCCAG	GAGGAAAAAG	GCATCAAGTA	TAAGTTGAA	4500
	GTCTACGAGA	AGAAAGACTA	ACAGGAAGAT	GCTTCAAGT	TCTCTGCTCC	CCTCCTAAAG	4560
	CTATGCATTT	TTATAAGACC	ATGGGACTTT	TGCTGGCTTT	AGATCAGCCT	CGACTGTGCC	4620
50	TTCTAGTTGC	CAGCCATCTG	TTGTTTGCCTC	CTCCCCGTG	CCTTCCTGAA	CCCTGGAAGG	4680
	TGCCACTCCC	ACTGTCCTTT	CCTAATAAAA	TGAGGAAATT	GCATCGCATT	GTCTGAGTAG	4740
	GTGTCATTCT	ATTCTGGGGG	GTGGGGTGGG	GCAGGACAGC	AAGGGGGAGG	ATTGGGAAGA	4800
55	CAATAGCAGG	CATGCTGGGG	ATCCGGTGGG	CTCTATGGAA	CCAGCTGGGG	CTCGAGCTAC	4860
	TAGCTTGCT	TCTCAATTTC	TTATTCGCAT	AATGAGAAAAA	AAAGGAAAT	TAATTTAAC	4920
60	ACCAATTCACT	TAGTTGATTG	ACCAATTGGG	TTGCCAAAAAA	GGATGCTTTA	GAGACAGTGT	4980
	TCTCTGCACA	GATAAGGACA	AACATTATTTC	AGAGGGAGTA	CCCAGAGCTG	AGACTCCTAA	5040

	GCCAGTGAGT	GGCACAGCAT	TCTAGGGAGA	AATATGCTTG	TCATCACCGA	AGCCTGATTC	5100
	CGTAGAGCCA	CACCTTGGTA	AGGGCCAATC	TGCTCACACA	GGATAGAGAG	GGCAGGAGCC	5160
5	AGGGCAGAGC	ATATAAGGTG	AGGTAGGATC	AGTTGCTCCT	CACATTTGCT	TCTGACATAG	5220
	TTGTGTTGGG	AGCTTGGATC	GATCCTCTAT	GGTTGAACAA	GATGGATTGC	ACGCAGGTTC	5280
10	TCCGGCCGCT	TGGCTGGAGA	GGCTATTGCG	ATATGACTGG	GCACAAEAGA	CAATCGACTG	5340
	CTCTGATGCC	GCCGTGTTCC	GGCTGTCAGC	GCAGGGCGC	CCGGTTCTTT	TTGTCAAGAC	5400
	CGACCTGTCC	GGTGCCTCTGA	ATGAACTGCA	GGACGGAGGA	GCGCGCTAT	CGTGGCTGGC	5460
15	CACGACGGGC	GTTCCCTTGC	CAGCTGTGCT	CGACGTTGTC	ACTGAAGCGG	GAAGGGACTG	5520
	GCTGCTATTG	GGCGAAGTGC	CGGGGCAGGA	TCTCCTGTCA	TCTCACCTTG	CTCCTGCCGA	5580
20	GAAAGTATCC	ATCATGGCTG	ATGCAATGCG	GGGGCTGCAT	ACGCTTGATC	CGGCTACCTG	5640
	CCCATTGAC	CACCAAGCGA	ACATCGCAT	CGAGCGAGCA	CGTACTCGGA	TGGAAGCCGG	5700
	TCTTGTCGAT	CAGGATGATC	TGGACGAAGA	GCATCAGGGG	CTCGCGCCAG	CCGAACTGTT	5760
25	CGCCAGGCTC	AAGGCGCGCA	TGCCCACGG	CGAGGATCTC	GTCGTGACCC	ATGGCGATGC	5820
	CTGCTTGCCG	AATATCATGG	TGGAAAATGG	CCGCTTTCT	GGATTCATCG	ACTGTGGCCG	5880
30	GCTGGGTGTG	GC GGACCGCT	ATCAGGACAT	AGCGTTGGCT	ACCCGTGATA	TTGCTGAAGA	5940
	GCTTGGCGGC	GAATGGGCTG	ACCGCTTCCT	CGTGCTTTAC	GGTATCGCCG	CTCCCGATTC	6000
	GCAGCGCATH	GCCTTCTATC	GCCTTCTTGA	CGAGTTCTTC	TGAGCGGGAC	TCTGGGTTC	6060
35	GAAATGACCG	ACCAAGCGAC	GCACCAACCTG	CCATCACGAG	ATTCGATTC	CACCGCCGCC	6120
	TTCTATGAAA	GGTTGGGCTT	CGGAATCGTT	TTCCGGGACG	CCGGCTGGAT	GATCCTCCAG	6180
40	CGCGGGGATC	TCATGCTGGA	GTTCTTCGCC	CACCCCAACT	TGTTTATTGC	AGCTTATAAT	6240
	GGTTACAAAT	AAAGCAATAG	CATCACAAAT	TTCACAAATA	AAGCATTTC	TTCACTGCAT	6300
	TCTAGTTGTG	GTTTGTCCAA	ACTCATCAAT	CTATCTTATC	ATGTCTGGAT	CGCGGCCGCG	6360
45	ATCCCCTCGA	GAGCTGGCG	TAATCATGGT	CATAGCTGTT	TCCTGTGTGA	AATTGTTATC	6420
	CGCTCACAAT	TCCACACAAC	ATACGAGCCG	GAAGCATAAA	GTGTAAAGCC	TGGGGTGCCT	6480
50	AATGAGTGAG	CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCGCTTTC	CAGTCGGAA	6540
	ACCTGTCGTG	CCAGCTGCAT	TAATGAATCG	GCCAACCGCG	GGGGAGAGGC	GGTTTGCCTA	6600
	TTGGGCCTC	TTCCGCTTCC	TCGCTCACTG	ACTCGCTGCG	CTCGGTCGTT	CGGCTGCCG	6660
55	GAGCGGTATC	AGCTCACTCA	AAGGCGGTAA	TACGGTTATC	CACAGAATCA	GGGGATAACG	6720
	CAGGAAAGAA	CATGTGAGCA	AAAGGCCAGC	AAAAGGCCAG	GAACCGTAAA	AAGGCCCGGT	6780
60	TGCTGGCGTT	TTTCCATAGG	CTCCGCCCTC	CTGACGAGCA	TCACAAAAAT	CGACGCTCAA	6840
	GTCAGAGGTG	GCGAAACCCG	ACAGGACTAT	AAAGATACCA	GGCGTTCCC	CCTGGAAGCT	6900
	CCCTCGTGCG	CTCTCCTGTT	CCGACCCCTGC	CGCTTACCGG	ATACCTGTCC	GCCTTCTCC	6960

	CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTTAGG	7020
5	TCGTTCGCTC CAAGCTGGC TGTGTGCACG AACCCCCGT TCAGCCGAC CGCTGCGCCT	7080
	TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG	7140
	<del>CAACCAACTCG TAACACQATT AACACACACAA AATATAATAAA CAAATACTACA GAATTCCTGA</del>	7200
10	AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGC'TGA	7260
	AGCCAGTTAC CTTCGAAAAA AGAGTTGGTA GCTCTTGATC CGGCAAACAA ACCACCGCTG	7320
15	GTAGCGGTGG TTTTTTGTT TGCAAGCAGC AGATTACGCG CAGAAAAAAA GGATCTCAAG	7380
	AAGATCCTTT GATCTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAC TCACGTTAAG	7440
	GGATTTGGT CATGACATTA TCAAAAAGGA TCTTCACCTA GATCCTTTA AATTAAAAAT	7500
20	GAAGTTTAA ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT	7560
	TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTCG TTCATCCATA GTTGCCTGAC	7620
25	TCCCCGTCGT GTAGATAACT ACGATAACGGG AGGGCTTACC ATCTGGCCCC AGTGCCTGCAA	7680
	TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTATC AGCAATAAAC CAGCCAGCCG	7740
	GAAGGGCCGA GCGCAGAAGT GGTCCCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAAATT	7800
30	GTTGCCGGGA AGCTAGACTA AGTAGTTCGC CAGTTAATAG TTTGCGAAC GTTGTGCCA	7860
	TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTGGTAT GGCTTCATTC AGCTCCGGTT	7920
35	CCCAACGATC AAGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAAGCG GTTAGCTCCT	7980
	TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG	8040
	CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTCT GTGACTGGTG	8100
40	AGTACTCAAC CAAGTCATTC TGAGAAATAGT GTATCGGGCG ACCGAGTTGC TCTTGCCTGG	8160
	CGTCAATAACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCCT ATCATTGGAA	8220
45	AACGTTCTTC GGGCGAAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTCGATGT	8280
	AACCCACTCG TGCACCCAACTGATCTTCAG CATCTTTAC TTTCACCAGC GTTTCTGGGT	8340
	GAGCAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT	8400
50	GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA	8460
	TGAGCGGATA CATATTGAA TGTATTTAGA AAAATAAACAA AATAGGGGTT CCGCGCACAT	8520
55	TTCCCCGAAAA AGTGCACCT	8540

(3) INFORMATION FOR SEQ ID NO: 2:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9209 bases

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: *no*

10 (iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15	GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG	60
	AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC	120
	GGAGAATGGG CGGAACCTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT	180
20	ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCACTTC TGCTGCTGG GGAGCCTGGG	240
	GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT	300
	GGGGAGCCTG GGGACTTTCC ACACCCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT	360
25	AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC	420
	GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG	480
30	ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA	540
	TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGT A TCATATGCCA	600
35	AGTACGCCCT CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT TGCCCACTAC	660
	ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC	720
	ATGGTGATGC GGTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGA	780
40	TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG	840
	GACTTTCCAA AATGTCGTA CAACCTCCGCC CCATTGACGC AAATGGCGG TAGGCGTGT	900
45	CGGTGGGAGG TCTATATAAG CAGACCTGGG TACGTGAACC GTCAGATCCG CTGGAGACGC	960
	CATCACAGAT CTCTCACTAT GGATTTCAG GTGCAGATT TCAGCTTCCT GCTAATCAGT	1020
	GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT	1080
50	GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTCAAGTGT AAGTTACATC	1140
	CACTGGTTCC AGCAGAAGCC AGGATCCCTT CCCAAACCTT GGATTTATGC CACATCCAAC	1200
55	CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTACTCTCTC	1260
	ACAATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT	1320
	AACCCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCCACCA	1380
60	TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCTGTTGTG	1440

	TGCCTGCTGA ATAACCTCTA	TCCCAGAGAG GCCAAAGTAC	AGTGGAAAGGT GGATAACGCC	1500
	CTCCAATCGG GTAACCTCCA	GGAGAGTGTC ACAGAGCAGG	ACAGCAAGGA CAGCACCTAC	1560
5	AGCCTCAGCA GCACCCCTGAC	GCTGAGCAAA GCAGACTACG	AGAAACACAA AGTCTACGCC	1620
	TGCGAAGTCA CCCATCAGGG	CCTGAGCTCG CCCGTCACAA	AGAGCTTCAA CAGGGGAGAG	1680
10	TGTTGAATTC AGATCCGTTA	ACGGTTACCA ACTACCTAGA	CTGGATTCTGT GACAACATGC	1740
	GGCCGTGATA TCTACGTATG	ATCAGCCTCG ACTGTGCCTT	CTAGTTGCCA GCCATCTGTT	1800
	TTTGCCCCCT CCCCCGTGCC	TTCCCTTGACC CTGGAAGGTG	CCACTCCCAC TGTCCTTTCC	1860
15	TAATAAAATG AGGAAATTGC	ATCGCATTGT CTGAGTAGGT	GTCATTCTAT TCTGGGGGGT	1920
	GGGGTGGGGC AGGACAGCAA	GGGGGAGGAT TGGGAAGACA	ATAGCAGGCA TGCTGGGGAT	1980
20	GCGGTGGGCT CTATGGAACC	AGCTGGGCT CGACAGCTAT	GCCAAGTACG CCCCCCTATTG	2040
	ACGTCAATGA CGGTAAATGG	CCCGCCTGGC ATTATGCCA	GTACATGACC TTATGGACT	2100
	TTCCTACTTG GCAGTACATC	TACGTATTAG TCATCGCTAT	TACCATGGTG ATGCGGTTTT	2160
25	GGCAGTACAT CAATGGGCGT	GGATAGCGGT TTGACTCACG	GGGATTTCGA AGTCTCCACC	2220
	CCATTGACGT CAATGGGAGT	TTGTTTGCG ACCAAAATCA	ACGGGACTTT CCAAAATGTC	2280
30	GTAACAACTC CGCCCCATTG	ACGCAAATGG GCGGTAGGCG	TGTACGGTGG GAGGTCTATA	2340
	TAAGCAGAGC TGGGTACGTC	CTCACATTCA GTGATCAGCA	CTGAACACAG ACCCGTCGAC	2400
	ATGGGTTGGA GCCTCATCTT	GCTCTTCCTT GTCGCTGTTG	CTACCGGTGT CCTGTCCCAG	2460
35	GTACAACATGC AGCAGCCTGG	GGCTGAGCTG GTGAAGCCTG	GGGCCTCAGT GAAGATGTCC	2520
	TGCAAGGCTT CTGGCTACAC	ATTTACCACT TACAATATGC	ACTGGGTAAA ACAGACACCT	2580
40	GGTCGGGGCC TGGAATGGAT	TGGAGCTATT TATCCCGAA	ATGGTGATAC TTCCCTACAAT	2640
	CAGAAGTTCA AAGGCAAGGC	CACATTGACT GCAGACAAAT	CCTCCAGCAC AGCCTACATG	2700
	CAGCTCAGCA GCCTGACATC	TGAGGACTCT CGGGTCTATT	ACTGTGCAAG ATCGACTTAC	2760
45	TACGGCGGTG ACTGGTACTT	CAATGCTCTGG GGCGCAGGG	CCACGGTCAC CGTCTCTGCA	2820
	GCTAGCACCA AGGGCCCATC	GGTCTTCCCC CTGGCACCC	CCTCCAAGAG CACCTCTGGG	2880
50	GGCACAGCGG CCCTGGGCTG	CCTGGTCAAG GACTACTTCC	CCGAACCGGT GACGGTGTG	2940
	TGGAACTCAG GCGCCCTGAC	CAGCGGGGTG CACACCTTCC	CGGCTGTCCT ACAGTCCTCA	3000
	GGACTCTACT CCCTCAGCAG	CGTGGTCACC GTGCCCTCCA	GCAGCTTGGG CACCCAGACC	3060
55	TACATCTGCA ACGTGAATCA	CAAGCCCCAG AACACCAAGG	TGGACAAGAA AGCAGAGCCC	3120
	AAATCTTGTG ACAAAACTCA	CACATGCCCA CCGTCCCCAG	CACCTGAACT CCTGGGGGG	3180
60	CCGTCAGTCT TCCTCTTCCC	CCCAAAACCC AAGGACACCC	TCATGATCTC CCGGACCCCT	3240
	GAGGTACAT GCGTGGTGGT	GGACGTGAGC CACGAAGACC	CTGAGGTCAA GTTCAACTGG	3300
	TACGTGGACG GCGTGGAGGT	GCATAATGCC AAGACAAAGC	CGCGGGAGGA GCAGTACAAC	3360

	AGCACGTACC	GTGTGGTCAG	CGTCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	3420
5	GAGTACAAGT	GCAAGGTCTC	CAACAAAGCC	CTCCCAGCCC	CCATCGAGAA	AACCATCTCC	3480
	AAAGCCAAAG	GGCAGCCCCG	AGAACACACAG	GTGTACACCC	TGCCCCCATC	CCGGGATGAG	3540
	CTGACCAAGA	ACCGACCTCA	CCTGACCTCC	CTGACCTAAAG	GTGTCTATCC	GGGGACATG	3600
10	GCCGTGGAGT	GGGAGAGCAA	TGGGCAGCCG	GAGAACAACT	ACAAGACCAC	GCCTCCCGTG	3660
	CTGGACTCCG	ACGGCTCCTT	CTTCCTCTAC	AGCAAGCTCA	CCGTGGACAA	GAGCAGGTGG	3720
15	CAGCAGGGGA	ACGTCTTCTC	ATGCTCCGTG	ATGCATGAGG	CTCTGCACAA	CCACTACACG	3780
	CAGAAGAGCC	TCTCCCTGTC	TCCGGGTAAA	TGAGGATCCG	TTAACGGTTA	CCAACTACCT	3840
	AGACTGGATT	CGTGACAACA	TGCGGCCGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
20	CTTCTAGTTG	CCAGCCATCT	GTTGTTGCC	CCTCCCCGT	GCCTTCCTTG	ACCCCTGGAAG	3960
	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	4020
25	GGTGTCAATT	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
	GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTCTT	ATTTGCATAA	TGAGAAAAAA	4200
30	AGGAAAATTA	ATTTAACAC	CAATTCACTA	GTTGATTGAG	CAAATGCCTT	GCCAAAAGG	4260
	ATGCTTTAGA	GACAGTGTTC	TCTGCACAGA	TAAGGACAAA	CATTATTCAG	AGGGAGTACC	4320
	CAGAGCTGAG	ACTCCTAACG	CAGTCAGTGG	CACACCATTC	TAGGGAGAAA	TATGCTTGTC	4380
35	ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAAG	GGCCAATCTG	CTCACACAGG	4440
	ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
40	CATTTGCTTC	TGACATAGTT	GTGTTGGAG	CTTGGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
	ATTCGCGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATT	TATCCCCGCT	4620
45	GCCATCATGG	TTCGACCATT	GAACTGCATC	GTCGCCGTGT	CCCCAAATAT	GGGGATTGGC	4680
	AAGAACGGAG	ACCTACCCCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
	ACCACAAACCT	CTTCAGTGGA	AGGTAAACAG	AATCTGGTGA	TTATGGGTAG	GAAAACCTGG	4800
50	TTCTCCATT	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
	GAACCTCAAAG	AACCACACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTGGA	TGATGCCTTA	4920
55	AGACTTATTG	AAACAACCGA	ATTGGCAAGT	AAAGTAGACA	TGGTTGGAT	AGTCGGAGGC	4980
	AGTTCTGTTT	ACCAGGAAGC	CATGAATCAA	CCAGGCCACC	TTAGACTCTT	TGTGACAAGG	5040
	ATCATGCAGG	AATTTGAAAG	TGACACGTT	TTCCCAGAA	TTGATTTGGG	GAAATATAAA	5100
60	CTTCTCCAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAAGG	CATCAAGTAT	5160
	AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTTCAAGTT	CTCTGCTCCC	5220

	CTCCTAAAGC TATGCATTT TATAAGACCA TGGGACTTTT GCTGGCTTTA GATCAGCCTC	5280
	GA C T G T G C C T T C T A G T T G C C AGCCATCTGT T G T T T G C C C C T C C C C G T G C C T T G A C	5340
5	CCTGGAAAGGT G C C A C T C C C A C T G T C C T T C T C T A A T A A A A T G A G G A A A T G C A T C G C A T T G	5400
	T C T G A G T A G G T G T C A T T C T A T T C T G G G G G T G G G G G C A G G A C A G C A A G G G G A G G A	5460
10	T T C G G A A A G A C A A T A G C A G G C A T G C T G G G G A T G C C G G G G C T C T A T G G A A C C A G C T G G G G C	5520
	T C G A G C T A C T A G C T T G C T T C T C A A T T C T A T T T G C A T A T G A G A A A A A A G G A A A T T	5580
15	A A T T T A A C A C C A A T C A G T A G T G A T T G A G C A A T G C G T T G C A A A A A A G C A T G C T T T A G	5640
	A G A C A G T G T T C T C T G C A C A G A T A A G G A C A A A C A T T A T T C A G A G G A G T A C C C A G A G C T G A	5700
	G A C T C C T A A G C C A G T G A G T G G C A T T G A T T G A A A T A T G C T T G T G A C A C C G A A	5760
20	G C C T G A T T C C T G A G G C A C A C C T T G G T A A G G C C A A T C T G C A C A C A G G A T A G A G A G G	5820
	G C A G G A G G C A A G G C A G A G C A T A A G G T G A G G A T G A T C A G T G C T C T C A C T T G C T T	5880
	C T G A C A T A G T T G T G T G G G A G C T T G G A T C G A T C T A T G G A A C A A G A T G G A T T G C A	5940
25	C C G A G G T T C T C C G G C G T T G G G A G A G G C T A T T C G G C T A T G A C T G G G C A C A A C A G A C	6000
	A A T C G G C T G C T C T G A T G C C C C C G T G T T C C G G C T G C A G C G C G C C C G G T T C T T T T	6060
30	T G T C A A G A C C G A C C T G T C C G G T G C C T G A A T G C A G G A G G C A G C G G C T A T C	6120
	G T G G C T G G C C A C G A C G G G C G T T C C T T G C G C A G C T G C T G C A G C T G T G C A C T G C G G G	6180
	A A C G G A C T G G C T G A T T G G G C G A A G T G C C G G G C A G G A T C T C C T G T C A T C T C A C C T T G C	6240
35	T C C T G C C G A G A A A G T A T C C A T G A T G G C T G A T G C A A T G C G G C G G C T G C A T A C G T G A T C C	6300
	G G C T A C C T G C C A C T T C G A C C A A G C G A A A C A T C G C A T C G A G G A G C A C G T A C T C G G A T	6360
40	G G A A G C C G G T C T T G T C G A T C A G G A T G A T C T G G A C A A G A G G A T C A G G G G C T C G C G C C A G C	6420
	C G A A C T G T T C C A G G C T C A A G G C G C A T G C C G A C G G C G G A G G A T C T C G T G A C C C A	6480
	T G G C G A T G C C T G C T G A T A T C A T G G T G G A A A A T G G C C G C T T T C T G G A T C A T C G A	6540
45	C T G T G G C C G G C G G A C C G C T A T C A G G A C A T A G C T G G C T A C C C G T G A T A T	6600
	T G C T G A A G A G C T T G G C G G A A T G G G C T G A T G C A T C T T G C C T G T T T A C G G T A C G C C G C	6660
50	T C C C G A T T C G C A G C G C A T C G C C T T C T A T C G C A C T T C T G A C G A T T C T T C T G A G C G G G A C T	6720
	C T G G G G T T C G A A A T G A C C G A C C A A G C G A C G C C C A A C C T G C A T C A C G A G A T T C G A T T C C	6780
	A C C G C C G C C T T C T A T G A A A G G T G G C T T G G A C G C C G G C T G G A T G A T G	6840
55	A T C C T C C A G C G G G G A T C T C A T G C T G G A G G T T C C T C G C C C A C C C A A C T T G T T T A T T G C A	6900
	G C T T A T A A T G T T A C A A A T A A G C A A T A G C A T C A C A A A T T T C A C A A A T A A A G C A T T T T T T	6960
60	T C A C T G C A T T C T A G T T G T G G G T T G T C C A A A C T C A T C A A T C T A T C T T A T C A T G C T G G A T C	7020
	G C G G C C G C G A T C C C G T C G A G A G C T T G G C G T A A T C A T G G T C A T G C T G T T T C C T G T G A A A	7080
	A T T G T T A T C C G C T C A C A A T T C C A C A C A A C A T A C G A G C C C G G A A G C A T A A A G G T A A A G C C T	7140

	GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTCC	7200
5	AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG	7260
	GTTTGCCTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTGTTTC	7320
	AGCTAAGCG ACCGCTATGA AGCTCACTCAA AGGGGGTAAT AGCGTTATCC AGACAAATCAG	7380
10	GGGATAACGC AGGAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA	7440
	AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCGCC TGACGAGCAT CACAAAATC	7500
15	GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTCCCC	7560
	CTGGAAGCTC CCTCGTGCAGC TCTCCTGTT CGACCCCTGCC GCTTACCGGA TACCTGTCCG	7620
	CCTTCCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT	7680
20	CGGTGTAGGT CGTCGCTCC AAGCTGGGCT GTGTGACGA ACCCCCCGTT CAGCCCGACC	7740
	GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAAGACAC GACTTATCGC	7800
25	CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG	7860
	AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACCTAGAAG GACAGTATTT GGTATCTGCG	7920
	CTCTGCTGAA GCCAGTTACC TTGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA	7980
30	CCACCGCTGG TAGCGGTGGT TTTTTGTTT GCAAGCAGCA GATTACGCCG AGAAAAAAAG	8040
	GATCTCAAGA AGATCCTTTG ATCTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAAC	8100
35	CACGTTAAGG GATTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTAA	8160
	ATTAAAAATG AAGTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT	8220
	ACCAATGCTT AATCACTGAG GCACCTATCT CAGCGATCTG TCTATTCGT TCATCCATAG	8280
40	TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA	8340
	GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAAACC	8400
45	AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT	8460
	CTATTAATTG TTGCGGGAA GCTAGAGTAA GTAGTTGCGC AGTTAATAGT TTGCGCAACG	8520
	TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA	8580
50	GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG	8640
	TTAGCTCCTT CGGTCCCTCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA	8700
55	TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTCTG	8760
	TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGCGA CCGAGTTGCT	8820
	CTTGGCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA	8880
60	TCATTGGAAA ACGTTCTCG GGGCGAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA	8940
	GTTCGATGTA ACCCACTCGT GCACCCAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA	9000

TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060  
GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120  
5 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180  
CGCGCACATT TCCCCGAAAA GTGCCACCT 9209

10 (4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 54 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: *no*

(iv) ANTI-SENSE: no

25 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

30 5' ATC ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT  
TC 3'

52  
542  
1

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 30 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: *no*

(iv) ANTI-SENSE: yes

45 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

50 5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3'

30

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

55

5 (A) LENGTH: 384 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: *no*  
(iv) ANTI-SENSE: no  
(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

15 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC 51  
ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT 102  
20 GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA 153  
AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG 204  
ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC 255  
25 AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA 306  
GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG ACT AGT AAC CCA CCC ACG TTC 357  
30 GGA GGG GGG ACC AAG CTG GAA ATC AAA 384

35 (7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 27 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: *no*  
45 (iv) ANTI-SENSE: no  
(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50 5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3'

27

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 29 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: *no* *yes*

15 (iv) ANTI-SENSE: yes

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5' GGS TGT TGT GCT AGC TGM RGA GAC RGT GA 3' 29

20 (9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 420 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: *no* *yes*

35 (iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

40	ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC	51
	CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG	102
	GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC	153
45	AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA	204
	GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC	255
	AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC	306
50	AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA AGA TCG ACT	357
	TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC GCA GGG ACC ACG GTC	408
	ACC GTC TCT GCA	420